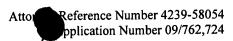
7; SEQ ID NO: 15; and SEQ ID NO: 17. Also encompassed within this invention are the isolated nucleic acid sequences that encode the carboxy-terminal conserved about 100 amino acids of the disclosed human-*P. carinii MSG*s; these may be used for amplification or as probes. The sequences of these conserved nucleic acid molecule regions include residues 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), or 1-249 of *HMSGp2* (SEQ ID NO: 15). In addition, this invention encompasses sequences with at least 70% sequence identity to these regions, and recombinant vectors comprising such nucleic acid molecules and conserved regions from within such nucleic acid molecules, as well as transgenic cells including such a recombinant vector.

Please replace the paragraph at page 3, lines 14-31 with the following:

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Another aspect of this invention provides a method of detecting the presence of Pneumocystis carinii in a biological specimen, by amplifying with a nucleic acid amplification method (e.g., the polymerase chain reaction) a human-P. carinii nucleic acid sequence using two or more oligonucleotide primers derived from a human-P. carinii MSG protein encoding sequence, then determining whether an amplified sequence is present. In a preferred embodiment of this invention, the human-R. carinii nucleic acid sequence is a highly conserved region within an MSG-protein encoding sequence. Such a highly conserved region may, for instance, include residues 2894-3042 of HM\$Gp1 (SEQ ID NO: 1), 2758-3006 of HM\$Gp3 (SEQ ID NO: 3), 2845-3090 of HMSG11 (SEQ ID NO: 5), 2839-3084 of HMSG14 (SEQ ID NO: 7), 2836-3081 of HMSG32 (SEQ ID NO: 9), 2887-3054 of HMSG33 (SEQ ID NO: 11), 2821-3072 of HMSG35 (SEQ ID NO: 13), or 1\249 of HMSGp2 (SEQ ID NO: 15). A further aspect of this invention is the method of detecting the presence of Pneumocystis carinii in a biological specimen, by determining whether an amplified sequence is present, for instance by electrophoresis and staining of the amplified sequence, or hybridization to a labeled probe of the amplified sequence. Appropriate labels for the hybridization probe include a fluorescent molecule, a chemiluminescent molecule, an enzyme a co-factor, an enzyme substrate, or a hapten. The nucleotide sequence of such a probe can be chosen from any MSG gene sequence



that is amplified in the detection method, and for instance can include a nucleic acid sequence according to SEQ ID NO: 19.

Please replace the paragraph at page 8, lines 28-33 with the following:

Further nucleic acid molecules might comprise at least 15 consecutive nucleotides of the regions encoding the conserved carboxy-terminal portion of each human-*P. carinii MSG* gene. These regions comprise nucleotides 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15), respectively.

Please replace the paragraph at page 12, line 35, through page 13, line 13 with the following:

Oligonucleotides that are derived from the human-P. carinii HMSGp1, HMSGp3, HMSG11, HMSG14, HMSG32, HMSG33, and HMSG35 gene sequences (SEQ ID NOS: 1, 3, 5, 7, 9, 11, and 13, respectively), as well as the fragment of HMSGp2 disclosed (SEQ ID NO: 15), are encompassed within the scope of the present invention. Preferably, such oligonucleotide primers will comprise a sequence of at least 15-20 consecutive nucleotides of the relevant human-P. carinii MSG gene sequence. To enhance amplification specificity, oligonucleotide primers comprising at least 25, 30, 35, 40, 45 or 50 consecutive nucleotides of these sequences may also be used. These primers for instance may be obtained from any region of the disclosed sequences. By way of example, human-R. carinii MSG gene sequences may be apportioned into halves or quarters based on sequence length, and the isolated nucleic acid molecules may be derived from the first or second halves of the molecules, or any of the four quarters. In addition, primers may be specifically chosen from the conserved carboxy-terminal region of each MSG coding sequence. This region comprises nucleic acid residues 2894-3042 of HMSGp1 (SEQ ID NO: 1), 2758-3006 of HMSGp3 (SEQ ID NO: 3), 2845-3090 of HMSG11 (SEQ ID NO: 5), 2839-3084 of HMSG14 (SEQ ID NO: 7), 28\$6-3081 of HMSG32 (SEQ ID NO: 9), 2887-3054 of HMSG33 (SEQ ID NO: 11), 2821-3072 of HMSG35 (SEQ ID NO: 13), and 1-249 of HMSGp2 (SEQ ID NO: 15).

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